



SEQUENCE LISTING

<110> Yarden, Yosef
Amit, Ido
Yakir, Liat

<120> POLYNUCLEOTIDES, POLYPEPTIDES AND ANTIBODIES AND USE THEREOF IN
TREATING TSG101-ASSOCIATED DISEASES

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<170> PatentIn version 3.5

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Leu Gln Gln Leu Leu Lys Glu Lys Lys Gln Arg Glu Glu Glu Leu His 770 775 780		
Gly Ile Leu Ala Glu Leu Glu Ala Lys Ser Glu Thr Lys Gln Glu Asn 785 790 795 800		
Tyr Trp Leu Ile Gln Tyr Gln Arg Leu Leu Asn Gln Lys Pro Leu Ser 805 810 815		
Leu Lys Leu Gln Glu Glu Gly Met Glu Arg Gln Leu Val Ala Leu Leu 820 825 830		
Val Glu Leu Ser Ala Glu His Tyr Leu Pro Leu Phe Ala His His Arg 835 840 845		
Ile Thr Leu Asp Met Leu Ser Arg Met Gly Pro Gly Asp Leu Ala Lys 850 855 860		
Val Gly Val Ser Glu Ala Gly Leu Gln His Glu Ile Leu Arg Arg Ala 865 870 875 880		
Arg Asp Leu Leu Asp Val Ala Arg Val Gln Pro Glu Leu Lys Pro Pro 885 890 895		
Lys Asn Glu Val Phe Gly Val Ser Glu Pro Pro Thr Ala Pro Gln Glu 900 905 910		
Leu Pro Glu Ser Val Arg Pro Ser Ala Pro Pro Ala Glu Leu Asp Val 915 920 925		
Pro Thr Ser Glu Cys Val Val Cys Leu Glu Arg Glu Ala Gln Met Val 930 935 940		
Phe Leu Thr Cys Gly His Val Cys Cys Cys Gln Gln Cys Cys Gln Pro 945 950 955 960		

Leu Arg Thr Cys Pro Leu Cys Arg Gln Glu Ile Ser Gln Arg Leu Arg
 965 970 975

Ile Tyr His Ser Ser
 980

<210> 7
 <211> 234
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Active portion of human Tal

<400> 7

Leu Lys Arg Lys Ser Leu Asp Thr Glu Ser Leu Gln Glu Met Ile Ser
 1 5 10 15

Glu Gln Arg Trp Ala Leu Ser Ser Leu Leu Gln Gln Leu Leu Lys Glu
 20 25 30

Lys Gln Gln Arg Glu Glu Glu Leu Arg Glu Ile Leu Thr Glu Leu Glu
 35 40 45

Ala Lys Ser Glu Thr Arg Gln Glu Asn Tyr Trp Leu Ile Gln Tyr Gln
 50 55 60

Arg Leu Leu Asn Gln Lys Pro Leu Ser Leu Lys Leu Gln Glu Glu Gly
 65 70 75 80

Met Glu Arg Gln Leu Val Ala Leu Leu Glu Glu Leu Ser Ala Glu His
 85 90 95

Tyr Leu Pro Ile Phe Ala His His Arg Leu Ser Leu Asp Leu Leu Ser
 100 105 110

Gln Met Ser Pro Gly Asp Leu Ala Lys Val Gly Val Ser Glu Ala Gly
 115 120 125

Leu Gln His Glu Ile Leu Arg Arg Val Gln Glu Leu Leu Asp Ala Ala
 130 135 140

Arg Ile Gln Pro Glu Leu Lys Pro Pro Met Gly Glu Val Val Thr Pro
 145 150 155 160

Thr Ala Pro Gln Glu Pro Pro Glu Ser Val Arg Pro Ser Ala Pro Pro
 165 170 175

Ala Glu Leu Glu Val Gln Ala Ser Glu Cys Val Val Cys Leu Glu Arg
 180 185 190

Glu Ala Gln Met Ile Phe Leu Asn Cys Gly His Val Cys Cys Cys Gln
 195 200 205

Gln Cys Cys Gln Pro Leu Arg Thr Cys Pro Leu Cys Arg Gln Asp Ile
 210 215 220

Ala Gln Arg Leu Arg Ile Tyr His Ser Ser
 225 230

<210> 8
 <211> 77
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Active portion of human Tal

<400> 8

Val Thr Pro Thr Ala Pro Gln Glu Pro Pro Glu Ser Val Arg Pro Ser
 1 5 10 15

Ala Pro Pro Ala Glu Leu Glu Val Gln Ala Ser Glu Cys Val Val Cys
 20 25 30

Leu Glu Arg Glu Ala Gln Met Ile Phe Leu Asn Cys Gly His Val Cys
 35 40 45

Cys Cys Gln Gln Cys Cys Gln Pro Leu Arg Thr Cys Pro Leu Cys Arg
 50 55 60

Gln Asp Ile Ala Gln Arg Leu Arg Ile Tyr His Ser Ser
 65 70 75

<210> 9
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Single strand DNA oligonucleotide

<400> 9
 ggaattcgtc atggcgggtgt cggag

25

<210> 10
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Single strand DNA oligonucleotide

<400> 10
 cctcgagtca gtagaggtca ctgagaccg

29

<210> 11
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide
 <400> 11
 ggaattcggg cttattcagg tcatgattg 29

<210> 12
 <211> 25
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Single strand DNA oligonucleotide
 <400> 12
 ccgggacatt cccacagctc cctta 25

<210> 13
 <211> 35
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Single strand DNA oligonucleotide
 <400> 13
 aaactgcagc cagagcagaa ctgagttctt catcc 35

<210> 14
 <211> 27
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Single strand DNA oligonucleotide
 <400> 14
 aaactgcagg gcacgatcca tttcctc 27

<210> 15
 <211> 19
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Single strand DNA oligonucleotide
 <400> 15
 cctgcagagc tggaggtgc 19

<210> 16
 <211> 20
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Single strand DNA oligonucleotide
 <400> 16
 gacgacctca cccattggtg 20

<210> 17
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Single strand DNA oligonucleotide
 <400> 17
 gtatgtatta cctctataag gcac 24

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Single strand DNA oligonucleotide
 <400> 18
 gggcttattc aggtcatgat tgt 23

<210> 19
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Single strand DNA oligonucleotide
 <400> 19
 cacaatcatg acctgaataa gcc 23

<210> 20
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Single strand DNA oligonucleotide
 <400> 20
 gaggacacca tccgagcctc 20

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Single strand DNA oligonucleotide
 <400> 21
 gaggctcgga tgggtgcctc 20

<210> 22
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Single strand DNA oligonucleotide
 <400> 22
 cattcccaca gctcccttat ac 22

<210> 23
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
<223> Single strand DNA oligonucleotide

<400> 23
gtataaggga gctgtgggaa tg

22

<210> 24
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Single strand DNA oligonucleotide

<400> 24
ggaggtggag actacaagga c

21

<210> 25
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Single strand DNA oligonucleotide

<400> 25
ccgggatcca tggcgggtgc ggag

24

<210> 26
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Single strand DNA oligonucleotide

<400> 26
atagtttagc ggccgctagt cacttgatcat cgtcgtc

37

<210> 27
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Single strand DNA oligonucleotide

<400> 27
cccaagcttg gaaggatgcc gctctt

26

<210> 28
<211> 61
<212> DNA
<213> Artificial sequence

<220>
<223> Single strand DNA oligonucleotide

<400> 28
ggggtacccc tcatcaggca taatcgggta catcataggg atagctgctg tggtagatgc

60

g

61

<210> 29

<211> 20
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 29
 ctcttcttgc agcttcaagg 20

 <210> 30
 <211> 18
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 30
 gccaggatcc agccagag 18

 <210> 31
 <211> 29
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 31
 cctcaactgt ggcgccgtct gctgctgcc 29

 <210> 32
 <211> 29
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 32
 ggcagcagca gacggcgcca cagttgagg 29

 <210> 33
 <211> 19
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 33
 cctgcagagc tggaggtgc 19

 <210> 34
 <211> 20
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 34
 gacgacctca cccattggtg 20

<210> 35
 <211> 19
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Single strand DNA oligonucleotide

<400> 35
 gaggagctgt cggctgagc

19

<210> 36
 <211> 27
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Single strand DNA oligonucleotide

<400> 36
 taacttaatc tggctcctga tctgccg

27

<210> 37
 <211> 19
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Active portion of human Tal

<400> 37

Val Thr Pro Thr Ala Pro Gln Glu Pro Pro Glu Ser Val Arg Pro Ser
 1 5 10 15

Ala Pro Pro

<210> 38
 <211> 700
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Active portion of human Tal

<400> 38
 aaagaggaag tccctggaca cagagtcact ccaggagatg atctcggagc agcgctgggc 60
 cctcagctcc ctgctccagc agctgctcaa agagaagcag cagcgagagg aagagctccg 120
 ggaaatcctg acggagttag aagccaaaag tgaaaccagg caggaaaatt actggctgat 180
 tcagtatcaa cggcttttga accagaagcc cttgtccttg aagctgcaag aagaggggat 240
 ggagcgccag ctggtggccc tcctggagga gctgtcggct gagcactacc tgcccatctt 300
 tgcgcaccac cgctctcac tggacctgct gagccaaatg agcccagggg acctggccaa 360
 ggtgggcgtc tcagaagctg gcctgcagca cgagatcctc cgagaggtcc aggaactgct 420
 ggtatgcagcc aggatccagc cagagctgaa accaccaatg ggtgaggtcg tcaccctac 480

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ggccccccag gagcctcctg agtctgtgag gccatccgct cccctgcag agctggaggt      540
gcaggcctca gagtgtgtcg tgtgcctgga acgggaggcc cagatgatct tcctcaactg      600
tggccacgtc tgctgtgcc agcagtgtcg ccagccactg cgcacctgcc cgctgtgccg      660
ccaggacatc gcccagcgcc tccgcatcta ccacagcagc      700

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<210> 39
<211> 231
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Active portion of human Tal

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<400> 39
gtcacccta cgcccccca ggagcctcct gagtctgtga ggccatccgc tccccctgca      60
gagctggagg tgcaggctc agagtgtgtc gtgtgcctgg aacgggaggc ccagatgatc      120
ttcctcaact gtggccacgt ctgtgtgtgc cagcagtgtc gccagccact gcgcacctgc      180
ccgtgtgcc gccaggacat cggccagcgc ctccgcatct accacagcag c      231

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<210> 40
<211> 55
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Active portion of human Tal

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<400> 40
gtcacccta cgcccccca ggagcctcct gagtctgtga ggccatccgc tcccc      55

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<210> 41
<211> 21
<212> DNA
<213> Artificial sequence

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<220>
<223> siRNA synthetic oligonucleotide

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<400> 41
ccuccagucu ucucucgu t      21

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<210> 42
<211> 21
<212> DNA
<213> Artificial sequence

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<220>
<223> siRNA synthetic oligonucleotide

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<400> 42
ttggagguca gaagagagca g      21

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<210> 43
<211> 21
<212> DNA
<213> Artificial sequence

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<220>
 <223> SiRNA synthetic oligonucleotide

 <400> 43
 guccaaaggu uccggagact t 21

 <210> 44
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> SiRNA synthetic oligonucleotide

 <400> 44
 ttcagguuuc caaggccucu g 21

 <210> 45
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> SiRNA synthetic oligonucleotide

 <400> 45
 ucaccucacu uccugcuut t 21

 <210> 46
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> SiRNA synthetic oligonucleotide

 <400> 46
 ttaguggagu gaaggacga a 21

 <210> 47
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> SiRNA synthetic oligonucleotide

 <400> 47
 ugcugacuga ggcuguaat t 21

 <210> 48
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> SiRNA synthetic oligonucleotide

 <400> 48
 uuacagcucu cagucagcat t 21

 <210> 49
 <211> 21
 <212> DNA

<213> Artificial sequence

<220>

<223> SiRNA synthetic oligonucleotide

<400> 49

aaugucgaga gucagucgut t

21

<210> 50

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> SiRNA synthetic oligonucleotide

<400> 50

acgacugacu cugacauut t

21

<210> 51

<211> 23

<212> PRT

<213> Artificial sequence

<220>

<223> PTAP-PSAP motif synthetic peptide GFP-fusion peptide

<400> 51

Glu Val Val Thr Pro Thr Ala Pro Gln Glu Pro Pro Glu Ser Val Arg
1 5 10 15

Pro Ser Ala Pro Pro Ala Glu
20

<210> 52

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 52

aagaattcag aggtcgtcac ccctacgg

28

<210> 53

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 53

aaggatccct ctgcaggggg agcgg

25

<210> 54

<211> 721

<212> PRT

<213> Ciona intestinalis

<400> 54

Met Pro Leu Gly Arg Phe Gly Ser Lys Lys Gln Ser Lys Asn Ala Lys

1	5	10	15
Arg Arg Phe Glu His Leu Met Val Met Ala Lys Glu Asn Pro Asp Arg	20	25	30
Ile Phe Asp Leu Ser Asp Cys Glu Leu His Glu Val Pro Asn Leu Met	35	40	45
Phe Ser Gln Cys Arg Val Leu Leu Thr Glu Ser Leu Leu Leu His Ser	50	55	60
Asn Leu Leu Lys Ser Leu Lys His Gly Gly Lys Met Ser Cys Leu Thr	65	70	75
Ser Leu Arg Val Leu Asp Leu His Asn Asn Arg Ile Ala Leu Leu Pro	85	90	95
Lys Asp Ile Gly Val Leu Ser Asn Leu Gln Val Phe Asn Ile Glu Asn	100	105	110
Asn Arg Ile Thr Glu Leu Pro Asp Ser Ile Gly Asp Leu Lys Lys Leu	115	120	125
Gln Ser Leu Leu Ala Lys Asp Asn Gln Leu Asn Ser Leu Pro Thr Thr	130	135	140
Ile Ser Gly Met Glu Ser Leu Arg Thr Leu Asp Ile Ser Gly Thr Asn	145	150	155
Lys Val Leu Tyr Leu Pro Lys Thr Leu Cys Lys Val Arg Thr Leu Glu	165	170	175
Val Phe Val Leu Ser Asn Pro Ala Val Met Glu Tyr Pro His Ser Met	180	185	190
Val Ala Cys Glu Gly Leu Glu Ala Ile Gln Lys Phe Ile Cys Lys Asp	195	200	205
Thr Gly Ile Glu Tyr Ile Pro Pro Ser His Ala Thr Leu Lys Val Leu	210	215	220
Asp Ser Ser Ala Thr Thr Ser Ser Ser Ser Lys Gln Thr Ala Ala Ala	225	230	235
Asn Leu Gln Leu Tyr Gln Ser Ser Met Asp Gln Tyr Gln Arg Ser Lys	245	250	255
Asp Glu Lys Met Lys Gln Gln Leu Glu Ile Glu Arg Ser Ile Ala Glu	260	265	270
Gln Gln Arg Glu Gln Ala Tyr Leu Thr Ala Lys Ala Lys His Glu Lys	275	280	285

Ala Lys Glu Asn Ala Phe Leu Lys Gln Glu Gln Ala Val Phe Asp Arg
 290 295 300
 Ser Ile Ser Glu Gln Gln Lys Lys Thr Glu Ile Glu Arg Gln Glu Met
 305 310 315 320
 Met Lys Thr Leu Thr Gln Val Glu Glu Glu Ala Ser Arg Leu Val Asn
 325 330 335
 Lys Leu Val Ser Met Asn Ile Gly Ala Lys Gln Arg Glu Glu Met Leu
 340 345 350
 Glu Gly Met Glu Arg Glu Arg Met Glu Gln Glu Glu Arg Phe Lys Val
 355 360 365
 Thr Gln Glu Asp Ile Asp Lys Leu Arg Lys Lys Glu Thr Leu Ala Ala
 370 375 380
 Met Gln Ser Val Leu Ala Asp Asn Ala His Tyr Ala Ile Ala Ile Lys
 385 390 395 400
 Lys Tyr Leu Gly Glu Gln Tyr His Met Thr Arg Gln Ala Gln Gln Thr
 405 410 415
 Leu Gly Ala Asp Asn Glu Leu Ile Glu His Glu Leu Lys Arg Gln Gln
 420 425 430
 Trp Asn Gln Gly Val Leu Val Asp Gln Ile Leu His Glu Glu Ser Leu
 435 440 445
 Gln Lys Glu Ala Phe Ile Met Leu Lys Leu Gln His Asp Ala Val Gln
 450 455 460
 Ala Arg Leu Val Asp Gln Ile Gly Gln Leu Gln Gly Glu Leu Ile Arg
 465 470 475 480
 Leu Thr Gln Ile Glu Ala Gln Arg Asn Lys His Arg Ile Asp Gln Asp
 485 490 495
 Lys Gln Thr Leu Ser Leu Ile Arg Asn Glu Leu Thr Asp Leu Leu Ile
 500 505 510
 Gln Leu Leu Lys Glu Lys Asp His Arg Glu Glu Met Val Lys Ser Arg
 515 520 525
 Leu Val Glu Met Glu Gln Gln Arg Glu Asp Asp Gln Val Asp Phe Trp
 530 535 540
 Leu Val Gln Tyr Gln Lys Leu Leu Asp Thr Lys Pro Glu Val Leu Val
 545 550 555 560
 Gln Lys Glu His Gly Val Asp Pro Gln Ile Val Arg Leu Leu Gln Arg
 565 570 575

Ser Asp Ala Ala His His Leu Ser Ala Phe Ala Arg His His Ile Thr
580 585 590

Met Asp Thr Ile Thr Thr Leu Asp Asp Glu Lys Leu Arg Ser Leu Gly
595 600 605

Val Phe Glu Ile Gly Leu Arg Glu Asn Ile Leu Arg Glu Ile Glu Glu
610 615 620

Leu Tyr Ile Gln Arg Lys Lys Val Asp Leu Pro Thr Ser Asp Glu Glu
625 630 635 640

His Pro Pro Pro Thr Ala Pro Val Glu Gln Ser Thr Ser Gln Asp Pro
645 650 655

Asp Val Val Gln Pro Thr Ala Pro Ser Glu Ser Gln Glu Glu Glu Asn
660 665 670

Glu Cys Val Val Cys Leu Asp Arg Asn Ser Asp Thr Ile Phe Leu Pro
675 680 685

Cys Gly His Val Cys Ala Cys Phe Ile Cys Ser Thr Gln Leu Gln Ser
690 695 700

Cys Pro Met Cys Arg Ser Asp Val Ala Gln Lys Ile Lys Ile Phe Arg
705 710 715 720

Ser

<210> 55
<211> 390
<212> PRT
<213> Artificial sequence

<220>
<223> Human derived WTTSG101

<400> 55

Met Ala Val Ser Glu Ser Gln Leu Lys Lys Met Val Ser Lys Tyr Lys
1 5 10 15

Tyr Arg Asp Leu Thr Val Arg Glu Thr Val Asn Val Ile Thr Leu Tyr
20 25 30

Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr Val Phe Asn Asp Gly Ser
35 40 45

Ser Arg Glu Leu Met Asn Leu Thr Gly Thr Ile Pro Val Pro Tyr Arg
50 55 60

Gly Asn Thr Tyr Asn Ile Pro Ile Cys Leu Trp Leu Leu Asp Thr Tyr
65 70 75 80

Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys Pro Thr Ser Ser Met Thr
 85 90 95
 Ile Lys Thr Gly Lys His Val Asp Ala Asn Gly Lys Ile Tyr Leu Pro
 100 105 110
 Tyr Leu His Glu Trp Lys His Pro Gln Ser Asp Leu Leu Gly Leu Ile
 115 120 125
 Gln Val Met Ile Val Val Phe Gly Asp Glu Pro Pro Val Phe Ser Arg
 130 135 140
 Pro Ile Ser Ala Ser Tyr Pro Pro Tyr Gln Ala Thr Gly Pro Pro Asn
 145 150 155 160
 Thr Ser Tyr Met Pro Gly Met Pro Gly Gly Ile Ser Pro Tyr Pro Ser
 165 170 175
 Gly Tyr Pro Pro Asn Pro Ser Gly Tyr Pro Gly Cys Pro Tyr Pro Pro
 180 185 190
 Gly Gly Pro Tyr Pro Ala Thr Thr Ser Ser Gln Tyr Pro Ser Gln Pro
 195 200 205
 Pro Val Thr Thr Val Gly Pro Ser Arg Asp Gly Thr Ile Ser Glu Asp
 210 215 220
 Thr Ile Arg Ala Ser Leu Ile Ser Ala Val Ser Asp Lys Leu Arg Trp
 225 230 235 240
 Arg Met Lys Glu Glu Met Asp Arg Ala Gln Ala Glu Leu Asn Ala Leu
 245 250 255
 Lys Arg Thr Glu Glu Asp Leu Lys Lys Gly His Gln Lys Leu Glu Glu
 260 265 270
 Met Val Thr Arg Leu Asp Gln Glu Val Ala Glu Val Asp Lys Asn Ile
 275 280 285
 Glu Leu Leu Lys Lys Lys Asp Glu Glu Leu Ser Ser Ala Leu Glu Lys
 290 295 300
 Met Glu Asn Gln Ser Glu Asn Asn Asp Ile Asp Glu Val Ile Ile Pro
 305 310 315 320
 Thr Ala Pro Leu Tyr Lys Gln Ile Leu Asn Leu Tyr Ala Glu Glu Asn
 325 330 335
 Ala Ile Glu Asp Thr Ile Phe Tyr Leu Gly Glu Ala Leu Arg Arg Gly
 340 345 350
 Val Ile Asp Leu Asp Val Phe Leu Lys His Val Arg Leu Leu Ser Arg
 355 360 365

Lys Gln Phe Gln Leu Arg Ala Leu Met Gln Lys Ala Arg Lys Thr Ala
 370 375 380

Gly Leu Ser Asp Leu Tyr
 385 390

<210> 56
 <211> 241
 <212> PRT
 <213> Artificial sequence

<220>
 <223> TSG101 delta N' truncation mutant

<400> 56

Tyr Pro Pro Tyr Gln Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro
 1 5 10 15

Gly Met Pro Gly Gly Ile Ser Pro Tyr Pro Ser Gly Tyr Pro Pro Asn
 20 25 30

Pro Ser Gly Tyr Pro Gly Cys Pro Tyr Pro Pro Gly Gly Pro Tyr Pro
 35 40 45

Ala Thr Thr Ser Ser Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val
 50 55 60

Gly Pro Ser Arg Asp Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser
 65 70 75 80

Leu Ile Ser Ala Val Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu
 85 90 95

Met Asp Arg Ala Gln Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu
 100 105 110

Asp Leu Lys Lys Gly His Gln Lys Leu Glu Glu Met Val Thr Arg Leu
 115 120 125

Asp Gln Glu Val Ala Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys
 130 135 140

Lys Asp Glu Glu Leu Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser
 145 150 155 160

Glu Asn Asn Asp Ile Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr
 165 170 175

Lys Gln Ile Leu Asn Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr
 180 185 190

Ile Phe Tyr Leu Gly Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp
 195 200 205

Val Phe Leu Lys His Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu
 210 215 220

Arg Ala Leu Met Gln Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu
 225 230 235 240

Tyr

<210> 57
 <211> 250
 <212> PRT
 <213> Artificial sequence

<220>
 <223> TSG101 delta C' truncation mutant

<400> 57

Met Ala Val Ser Glu Ser Gln Leu Lys Lys Met Val Ser Lys Tyr Lys
 1 5 10 15

Tyr Arg Asp Leu Thr Val Arg Glu Thr Val Asn Val Ile Thr Leu Tyr
 20 25 30

Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr Val Phe Asn Asp Gly Ser
 35 40 45

Ser Arg Glu Leu Met Asn Leu Thr Gly Thr Ile Pro Val Pro Tyr Arg
 50 55 60

Gly Asn Thr Tyr Asn Ile Pro Ile Cys Leu Trp Leu Leu Asp Thr Tyr
 65 70 75 80

Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys Pro Thr Ser Ser Met Thr
 85 90 95

Ile Lys Thr Gly Lys His Val Asp Ala Asn Gly Lys Ile Tyr Leu Pro
 100 105 110

Tyr Leu His Glu Trp Lys His Pro Gln Ser Asp Leu Leu Gly Leu Ile
 115 120 125

Gln Val Met Ile Val Val Phe Gly Asp Glu Pro Pro Val Phe Ser Arg
 130 135 140

Pro Ile Ser Ala Ser Tyr Pro Pro Tyr Gln Ala Thr Gly Pro Pro Asn
 145 150 155 160

Thr Ser Tyr Met Pro Gly Met Pro Gly Gly Ile Ser Pro Tyr Pro Ser
 165 170 175

Gly Tyr Pro Pro Asn Pro Ser Gly Tyr Pro Gly Cys Pro Tyr Pro Pro
 180 185 190

Gly Gly Pro Tyr Pro Ala Thr Thr Ser Ser Gln Tyr Pro Ser Gln Pro

195 200 205
 Pro Val Thr Thr Val Gly Pro Ser Arg Asp Gly Thr Ile Ser Glu Asp
 210 215 220
 Thr Ile Arg Ala Ser Leu Ile Ser Ala Val Ser Asp Lys Leu Arg Trp
 225 230 235 240
 Arg Met Lys Glu Glu Met Asp Arg Ala Gln
 245 250
 <210> 58
 <211> 303
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> TSG101 deltaSB truncation mutant
 <400> 58
 Met Ala Val Ser Glu Ser Gln Leu Lys Lys Met Val Ser Lys Tyr Lys
 1 5 10 15
 Tyr Arg Asp Leu Thr Val Arg Glu Thr Val Asn Val Ile Thr Leu Tyr
 20 25 30
 Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr Val Phe Asn Asp Gly Ser
 35 40 45
 Ser Arg Glu Leu Met Asn Leu Thr Gly Thr Ile Pro Val Pro Tyr Arg
 50 55 60
 Gly Asn Thr Tyr Asn Ile Pro Ile Cys Leu Trp Leu Leu Asp Thr Tyr
 65 70 75 80
 Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys Pro Thr Ser Ser Met Thr
 85 90 95
 Ile Lys Thr Gly Lys His Val Asp Ala Asn Gly Lys Ile Tyr Leu Pro
 100 105 110
 Tyr Leu His Glu Trp Lys His Pro Gln Ser Asp Leu Leu Gly Leu Ile
 115 120 125
 Gln Val Met Ile Val Val Phe Gly Asp Glu Pro Pro Val Phe Ser Arg
 130 135 140
 Pro Ile Ser Ala Ser Tyr Pro Pro Tyr Gln Ala Thr Gly Pro Pro Asn
 145 150 155 160
 Thr Ser Tyr Met Pro Gly Met Pro Gly Gly Ile Ser Pro Tyr Pro Ser
 165 170 175
 Gly Tyr Pro Pro Asn Pro Ser Gly Tyr Pro Gly Cys Pro Tyr Pro Pro
 180 185 190

Gly Gly Pro Tyr Pro Ala Thr Thr Ser Ser Gln Tyr Pro Ser Gln Pro
195 200 205

Pro Val Thr Thr Val Gly Pro Ser Arg Asp Gly Thr Ile Ser Glu Asp
210 215 220

Thr Ile Arg Ala Ser Leu Ile Ser Ala Val Ser Asp Lys Leu Arg Trp
225 230 235 240

Arg Met Lys Glu Glu Met Asp Arg Ala Gln Ala Glu Leu Asn Ala Leu
245 250 255

Lys Arg Thr Glu Glu Asp Leu Lys Lys Gly His Gln Lys Leu Glu Glu
260 265 270

Met Val Thr Arg Leu Asp Gln Glu Val Ala Glu Val Asp Lys Asn Ile
275 280 285

Glu Leu Leu Lys Lys Lys Asp Glu Glu Leu Ser Ser Ala Leu Glu
290 295 300

<210> 59
<211> 88
<212> PRT
<213> Artificial sequence

<220>
<223> TSG101SB truncation mutant

<400> 59

Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp Ile Asp Glu Val Ile
1 5 10 15

Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu Asn Leu Tyr Ala Glu
20 25 30

Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu Gly Glu Ala Leu Arg
35 40 45

Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys His Val Arg Leu Leu
50 55 60

Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met Gln Lys Ala Arg Lys
65 70 75 80

Thr Ala Gly Leu Ser Asp Leu Tyr
85

<210> 60
<211> 233
<212> PRT
<213> Artificial sequence

<220>
<223> Human derived Tal delta N' truncation mutant

<400> 60

Ile Glu Thr Glu Leu Leu Gln Leu Thr Gln Leu Glu Leu Lys Arg Lys
 1 5 10 15

Ser Leu Asp Thr Glu Ser Leu Gln Glu Met Ile Ser Glu Gln Arg Trp
 20 25 30

Ala Leu Ser Ser Leu Leu Gln Gln Leu Leu Lys Glu Lys Gln Gln Arg
 35 40 45

Glu Glu Glu Leu Arg Glu Ile Leu Thr Glu Leu Glu Ala Lys Ser Glu
 50 55 60

Thr Arg Gln Glu Asn Tyr Trp Leu Ile Gln Tyr Gln Arg Leu Leu Asn
 65 70 75 80

Gln Lys Pro Leu Ser Leu Lys Leu Gln Glu Glu Gly Met Glu Arg Gln
 85 90 95

Leu Val Ala Leu Leu Glu Glu Leu Ser Ala Glu His Tyr Leu Pro Ile
 100 105 110

Phe Ala His His Arg Leu Ser Leu Asp Leu Leu Ser Gln Met Ser Pro
 115 120 125

Gly Asp Leu Ala Lys Val Gly Val Ser Glu Ala Gly Leu Gln His Glu
 130 135 140

Ile Leu Arg Arg Val Gln Glu Leu Leu Asp Ala Ala Arg Ile Gln Pro
 145 150 155 160

Glu Leu Lys Pro Pro Met Gly Glu Val Val Thr Pro Thr Ala Pro Gln
 165 170 175

Glu Pro Pro Glu Ser Val Arg Pro Ser Ala Pro Pro Ala Glu Leu Glu
 180 185 190

Val Gln Ala Ser Glu Cys Val Val Cys Leu Glu Arg Glu Ala Gln Met
 195 200 205

Ile Phe Leu Asn Cys Gly His Val Cys Cys Cys Gln Gln Cys Cys Gln
 210 215 220

Pro Leu Arg Thr Cys Pro Leu Cys Arg
 225 230

<210> 61

<211> 134

<212> PRT

<213> Artificial sequence

<220>

<223> Human derived Tal-CC

<400> 61

Lys Leu Ile Glu Thr Glu Leu Leu Gln Leu Thr Gln Leu Glu Leu Lys
 1 5 10 15

Arg Lys Ser Leu Asp Thr Glu Ser Leu Gln Glu Met Ile Ser Glu Gln
 20 25 30

Arg Trp Ala Leu Ser Ser Leu Leu Gln Gln Leu Leu Lys Glu Lys Gln
 35 40 45

Gln Arg Glu Glu Glu Leu Arg Glu Ile Leu Thr Glu Leu Glu Ala Lys
 50 55 60

Ser Glu Thr Arg Gln Glu Asn Tyr Trp Leu Ile Gln Tyr Gln Arg Leu
 65 70 75 80

Leu Asn Gln Lys Pro Leu Ser Leu Lys Leu Gln Glu Glu Gly Met Glu
 85 90 95

Arg Gln Leu Val Ala Leu Leu Glu Glu Leu Ser Ala Glu His Tyr Leu
 100 105 110

Pro Ile Phe Ala His His Arg Leu Ser Leu Asp Leu Leu Ser Gln Met
 115 120 125

Ser Pro Gly Asp Leu Ala
 130

<210> 62

<211> 500

<212> PRT

<213> Artificial sequence

<220>

<223> HIV1 derived GAG protein

<400> 62

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
 1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
 20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
 35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
 50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
 85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
 100 105 110
 Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
 115 120 125
 Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
 130 135 140
 Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
 145 150 155 160
 Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
 165 170 175
 Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
 180 185 190
 Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
 195 200 205
 Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
 210 215 220
 Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
 225 230 235 240
 Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
 245 250 255
 Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
 260 265 270
 Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
 275 280 285
 Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
 290 295 300
 Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
 305 310 315 320
 Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
 325 330 335
 Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
 340 345 350
 Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser
 355 360 365
 Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg
 370 375 380

Asn Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His
385 390 395 400

Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys
405 410 415

Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn
420 425 430

Phe Leu Gly Lys Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe
435 440 445

Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg
450 455 460

Ser Gly Val Glu Thr Thr Thr Pro Pro Gln Lys Gln Glu Pro Ile Asp
465 470 475 480

Lys Glu Leu Tyr Pro Leu Thr Ser Leu Arg Ser Leu Phe Gly Asn Asp
485 490 495

Pro Ser Ser Gln
500

<210> 63
<211> 216
<212> PRT
<213> Artificial sequence

<220>
<223> Human derived Tal deltaP truncation mutant

<400> 63

Ile Glu Thr Glu Leu Leu Gln Leu Thr Gln Leu Glu Leu Lys Arg Lys
1 5 10 15

Ser Leu Asp Thr Glu Ser Leu Gln Glu Met Ile Ser Glu Gln Arg Trp
20 25 30

Ala Leu Ser Ser Leu Leu Gln Gln Leu Leu Lys Glu Lys Gln Gln Arg
35 40 45

Glu Glu Glu Leu Arg Glu Ile Leu Thr Glu Leu Glu Ala Lys Ser Glu
50 55 60

Thr Arg Gln Glu Asn Tyr Trp Leu Ile Gln Tyr Gln Arg Leu Leu Asn
65 70 75 80

Gln Lys Pro Leu Ser Leu Lys Leu Gln Glu Glu Gly Met Glu Arg Gln
85 90 95

Leu Val Ala Leu Leu Glu Glu Leu Ser Ala Glu His Tyr Leu Pro Ile
100 105 110

Phe Ala His His Arg Leu Ser Leu Asp Leu Leu Ser Gln Met Ser Pro
 115 120 125
 Gly Asp Leu Ala Lys Val Gly Val Ser Glu Ala Gly Leu Gln His Glu
 130 135 140
 Ile Leu Arg Arg Val Gln Glu Leu Leu Asp Ala Ala Arg Ile Gln Pro
 145 150 155 160
 Glu Leu Lys Pro Pro Met Gly Glu Val Val Pro Ala Glu Leu Glu Val
 165 170 175
 Gln Ala Ser Glu Cys Val Val Cys Leu Glu Arg Glu Ala Gln Met Ile
 180 185 190
 Phe Leu Asn Cys Gly His Val Cys Cys Cys Gln Gln Cys Cys Gln Pro
 195 200 205
 Leu Arg Thr Cys Pro Leu Cys Arg
 210 215